

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/521,174
Source: 1FWP
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IFWP

RAW SEQUENCE LISTING

DATE: 07/05/2006

PATENT APPLICATION: US/10/521,174

TIME: 13:48:42

Input Set : A:\Sequence Listing 8-26-05.txt

Output Set: N:\CRF4\07052006\J521174.raw

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3 <110> APPLICANT: AMANO, Yuichiro
4     SUGIYAMA, Yasuo
5     NISHIDA, Mayumi
6     TAKETOMI, Shigehisa
8 <120> TITLE OF INVENTION: Disease Model Animal Carrying Heterologous PPAR Alpha Gene
Introduced
9     Thereinto And Use Thereof
11 <130> FILE REFERENCE: 2005-0041A/WMC/00279
13 <140> CURRENT APPLICATION NUMBER: 10/521,174
14 <141> CURRENT FILING DATE: 2005-1-14
16 <150> PRIOR APPLICATION NUMBER: JP 2002-206162
17 <151> PRIOR FILING DATE: 2002-07-15
19 <160> NUMBER OF SEQ ID NOS: 9
21 <170> SOFTWARE: PatentIn version 3.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1404
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (1)..(1404)
33 <400> SEQUENCE: 1
34 atg gtg gac acg gaa agc cca ctc tgc ccc ctc tcc cca ctc gag gcc      48
35 Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
36 1          5          10          15
37 ggc gat cta gag agc ccg tta tct gaa gag ttc ctg caa gaa atg gga      96
38 Gly Asp Leu Glu Ser Pro Leu Ser Glu Phe Leu Gln Glu Met Gly
39          20          25          30
40 aac atc caa gag att tcg caa tcc atc ggc gag gat agt tct gga agc      144
41 Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
42          35          40          45
43 ttt ggc ttt acg gaa tac cag tat tta gga agc tgt cct ggc tca gat      192
44 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
45          50          55          60
46 ggc tcg gtc atc acg gac acg ctt tca cca gct tcg agc ccc tcc tcg      240
47 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
48 65          70          75          80
49 gtg act tat cct gtg gtc ccc ggc agc gtg gac gag tct ccc agt gga      288
50 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
51          85          90          95
52 gca ttg aac atc gaa tgt aga atc tgc ggg gac aag gcc tca ggc tat      336
53 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
54          100         105         110
55 cat tac gga gtc cac gcg tgt gaa ggc tgc aag ggc ttc ttt cgg cga      384

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56 His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
57      115      120      125
58 acg att cga ctc aag ctg gtg tat gac aag tgc gac cgc agc tgc aag      432
59 Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
60      130      135      140
61 atc cag aaa aag aac aga aac aaa tgc cag tat tgt cga ttt cac aag      480
62 Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
63 145      150      155      160
64 tgc ctt tct gtc ggg atg tca cac aac gcg att cgt ttt gga cga atg      528
65 Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
66      165      170      175
67 cca aga tct gag aaa gca aaa ctg aaa gca gaa att ctt acc tgt gaa      576
68 Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
69      180      185      190
70 cat gac ata gaa gat tct gaa act gca gat ctc aaa tct ctg gcc aag      624
71 His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
72      195      200      205
73 aga atc tac gag gcc tac ttg aag aac ttc aac atg aac aag gtc aaa      672
74 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
75      210      215      220
76 gcc cgg gtc atc ctc tca gga aag gcc agt aac aat cca cct ttt gtc      720
77 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
78 225      230      235      240
79 ata cat gat atg gag aca ctg tgt atg gct gag aag acg ctg gtg gcc      768
80 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
81      245      250      255
82 aag ctg gtg gcc aat ggc atc cag aac aag gag gcg gag gtc cgc atc      816
83 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
84      260      265      270
85 ttt cac tgc tgc cag tgc acg tca gtg gag acc gtc acg gag ctc acg      864
86 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
87      275      280      285
88 gaa ttc gcc aag gcc atc cca ggc ttc gca aac ttg gac ctg aac gat      912
89 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
90      290      295      300
91 caa gtg aca ttg cta aaa tac gga gtt tat gag gcc ata ttc gcc atg      960
92 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
93 305      310      315      320
94 ctg tct tct gtg atg aac aaa gac ggg atg ctg gta gcg tat gga aat      1008
95 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
96      325      330      335
97 ggg ttt ata act cgt gaa ttc cta aaa agc cta agg aaa ccg ttc tgt      1056
98 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
99      340      345      350
100 gat atc atg gaa ccc aag ttt gat ttt gcc atg aag ttc aat gca ctg      1104
101 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
102      355      360      365
103 gaa ctg gat gac agt gat atc tcc ctt ttt gtg gct gct atc att tgc      1152
104 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys

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105      370      375      380
106 tgt gga gat cgt cct ggc ctt cta aac gta gga cac att gaa aaa atg      1200
107 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
108 385      390      395      400
109 cag gag ggt att gta cat gtg ctc aga ctc cac ctg cag agc aac cac      1248
110 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
111      405      410      415
112 ccg gac gat atc ttt ctc ttc cca aaa ctt ctt caa aaa atg gca gac      1296
113 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
114      420      425      430
115 ctc cgg cag ctg gtg acg gag cat gcg cag ctg gtg cag atc atc aag      1344
116 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
117      435      440      445
118 aag acg gag tcg gat gct gcg ctg cac ccg cta ctg cag gag atc tac      1392
119 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
120      450      455      460
121 agg gac atg tac      1404
122 Arg Asp Met Tyr
123 465
125 <210> SEQ ID NO: 2
126 <211> LENGTH: 468
127 <212> TYPE: PRT
128 <213> ORGANISM: Homo sapiens
130 <400> SEQUENCE: 2
131 Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
132 1      5      10      15
133 Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
134      20      25      30
135 Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
136      35      40      45
137 Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
138      50      55      60
139 Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
140 65      70      75      80
141 Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
142      85      90      95
143 Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
144      100      105      110
145 His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
146      115      120      125
147 Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
148      130      135      140
149 Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
150 145      150      155      160
151 Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
152      165      170      175
153 Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
154      180      185      190
155 His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys

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```

156          195          200          205
157 Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
158          210          215          220
159 Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
160 225          230          235          240
161 Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
162          245          250          255
163 Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Ala Glu Val Arg Ile
164          260          265          270
165 Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
166          275          280          285
167 Glu Phe Ala Lys Ala Ile Pro Gly Phe Ala Asn Leu Asp Leu Asn Asp
168          290          295          300
169 Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
170 305          310          315          320
171 Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
172          325          330          335
173 Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
174          340          345          350
175 Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
176          355          360          365
177 Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
178          370          375          380
179 Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
180 385          390          395          400
181 Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
182          405          410          415
183 Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
184          420          425          430
185 Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
186          435          440          445
187 Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
188          450          455          460
189 Arg Asp Met Tyr
190 465

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192 <210> SEQ ID NO: 3

193 <211> LENGTH: 20

194 <212> TYPE: DNA

195 <213> ORGANISM: Artificial Sequence

197 <220> FEATURE:

198 <223> OTHER INFORMATION: Oligonucleotide designed to act as primer for amplifying

human

199 SAP promoter.

201 <400> SEQUENCE: 3

202 actgagtaga agtagcagaa

20

204 <210> SEQ ID NO: 4

205 <211> LENGTH: 20

206 <212> TYPE: DNA

207 <213> ORGANISM: Artificial Sequence

209 <220> FEATURE:

274 cccccggcag tgcctgaa

19

VERIFICATION SUMMARY

DATE: 07/05/2006

PATENT APPLICATION: US/10/521,174

TIME: 13:48:43

Input Set : A:\Sequence Listing 8-26-05.txt

Output Set: N:\CRF4\07052006\J521174.raw

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